



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/736,889

DATE: 09/01/2004

TIME: 12:49:14

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\09012004\J736889.raw

3 <110> APPLICANT: AURELIUM BIOPHARMA INC.
 5 <120> TITLE OF INVENTION: VIMENTIN DIRECTED DIAGNOSTICS AND THERAPEUTICS FOR
 6 MULTIDRUG RESISTANT NEOPLASTIC DISEASE
 8 <130> FILE REFERENCE: 112418.147US
 10 <140> CURRENT APPLICATION NUMBER: 10/736,889
 11 <141> CURRENT FILING DATE: 2003-12-15
 13 <150> PRIOR APPLICATION NUMBER: 60/433,480
 14 <151> PRIOR FILING DATE: 2002-12-13
 16 <160> NUMBER OF SEQ ID NOS: 5
 18 <170> SOFTWARE: PatentIn Ver. 3.2
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 466
 22 <212> TYPE: PRT
 23 <213> ORGANISM: Homo sapiens
 25 <400> SEQUENCE: 1
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 27 1 5 10 15
 29 Gly Pro Gly Thr Ala Ser Arg Pro Ser Ser Ser Arg Ser Tyr Val Thr
 30 20 25 30
 32 Thr Ser Thr Arg Thr Tyr Ser Leu Gly Ser Ala Leu Arg Pro Ser Thr
 33 35 40 45
 35 Ser Arg Ser Leu Tyr Ala Ser Ser Pro Gly Gly Val Tyr Ala Thr Arg
 36 50 55 60
 38 Ser Ser Ala Val Arg Leu Arg Ser Ser Val Pro Gly Val Arg Leu Leu
 39 65 70 75 80
 41 Gln Asp Ser Val Asp Phe Ser Leu Ala Asp Ala Ile Asn Thr Glu Phe
 42 85 90 95
 44 Lys Asn Thr Arg Thr Asn Glu Lys Val Glu Leu Gln Glu Leu Asn Asp
 45 100 105 110
 47 Arg Phe Ala Asn Tyr Ile Asp Lys Val Arg Phe Leu Glu Gln Gln Asn
 48 115 120 125
 50 Lys Ile Leu Leu Ala Glu Leu Glu Gln Leu Lys Gly Gln Gly Lys Ser
 51 130 135 140
 53 Arg Leu Gly Asp Leu Tyr Glu Glu Glu Met Arg Glu Leu Arg Arg Gln
 54 145 150 155 160
 56 Val Asp Gln Leu Thr Asn Asp Lys Ala Arg Val Glu Val Glu Arg Asp
 57 165 170 175
 59 Asn Leu Ala Glu Asp Ile Met Arg Leu Arg Glu Lys Leu Gln Glu Glu
 60 180 185 190
 62 Met Leu Gln Arg Glu Glu Ala Glu Asn Thr Leu Gln Ser Phe Arg Gln
 63 195 200 205
 65 Asp Val Asp Asn Ala Ser Leu Ala Arg Leu Asp Leu Glu Arg Lys Val
 66 210 215 220

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68 Glu Ser Leu Gln Glu Glu Ile Ala Phe Leu Lys Lys Leu His Glu Glu
69 225                230                235                240
71 Glu Ile Gln Glu Leu Gln Ala Gln Ile Gln Glu Gln His Val Gln Ile
72                245                250                255
74 Asp Val Asp Val Ser Lys Pro Asp Leu Thr Ala Ala Leu Arg Asp Val
75                260                265                270
77 Arg Gln Gln Tyr Glu Ser Val Ala Ala Lys Asn Leu Gln Glu Ala Glu
78                275                280                285
80 Glu Trp Tyr Lys Ser Lys Phe Ala Asp Leu Ser Glu Ala Ala Asn Arg
81                290                295                300
83 Asn Asn Asp Ala Leu Arg Gln Ala Lys Gln Glu Ser Thr Glu Tyr Arg
84 305                310                315                320
86 Arg Gln Val Gln Ser Leu Thr Cys Glu Val Asp Ala Leu Lys Gly Thr
87                325                330                335
89 Asn Glu Ser Leu Glu Arg Gln Met Arg Glu Met Glu Glu Asn Phe Ala
90                340                345                350
92 Val Glu Ala Ala Asn Tyr Gln Asp Thr Ile Gly Arg Leu Gln Asp Glu
93                355                360                365
95 Ile Gln Asn Met Lys Glu Glu Met Ala Arg His Leu Arg Glu Tyr Gln
96                370                375                380
98 Asp Leu Leu Asn Val Lys Met Ala Leu Asp Ile Glu Ile Ala Thr Tyr
99 385                390                395                400
101 Arg Lys Leu Leu Glu Gly Glu Glu Ser Arg Ile Ser Leu Pro Leu Pro
102                405                410                415
104 Asn Phe Ser Ser Leu Asn Leu Arg Glu Thr Asn Leu Asp Ser Leu Pro
105                420                425                430
107 Leu Val Asp Thr His Ser Lys Arg Thr Phe Leu Ile Lys Thr Val Glu
108                435                440                445
110 Thr Arg Asp Gly Gln Val Ile Asn Glu Thr Ser Gln His His Asp Asp
111                450                455                460
113 Leu Glu
114 465

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117 <210> SEQ ID NO: 2

118 <211> LENGTH: 1766

119 <212> TYPE: DNA

120 <213> ORGANISM: Homo sapiens

122 <400> SEQUENCE: 2

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125 cagccggagc tacgtgacta cgtccaccgc cacctacagc ctgggcagcg cgctgcgccc 180
126 cagcaccagc cgcagcctct acgctctgtc cccggggcggc gtgtatgccg cgcgctcctc 240
127 tgccgtgcgc ctgcggagca gcgtgcccgg ggtgcggctc ctgcaggact cgggtggactt 300
128 ctcgctggcc gacgccatca acaccgagtt caagaacacc cgcaccaacg agaaggtgga 360
129 gctgcaggag ctgaatgacc gtttcgcaa ctacatcgac aaggtgcgct tcctggagca 420
130 gcagaataag atcctgctgg ccgagctcga gcagctcaag ggccaaggca agtcgcgcct 480
131 gggggacctc tacgaggagg agatgcggga gctgcgccgg caggtggacc agctaaccac 540
132 cgacaaagcc cgcgtcgagg tggagcgcca caacctggcc gaggacatca tgcgcctccg 600
133 ggagaaattg caggaggaga tgcttcagag agaggaagcc gaaaacaccc tgcaatcttt 660
134 cagacaggat gttgacaatg cgtctctggc acgtcttgac cttgaacgca aagtgggaatc 720

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135 tttgcaagaa gagattgcct ttttgaagaa actccacgaa gaggaaatcc aggagctgca 780
136 ggctcagatt caggaacagc atgtccaaat cgatgtggat gtttccaagc ctgacctcac 840
137 ggctgccttg cgtgacgtac gtcagcaata tgaaagtgtg gctgccaaga acctgcagga 900
138 ggcagaagaa tggtaacaat ccaagtttgc tgacctctct gaggctgcca accggaacaa 960
139 tgacgccttg cgccaggcaa agcaggagtc cactgagtac cggagacagg tgcagtcctt 1020
140 cacctgtgaa gtggatgccc tttaaaggaac caatgagtc ctggaacgcc agatgcgtga 1080
141 aatggaagag aactttgccg ttgaagctgc taactaccaa gacactattg gccgcctgca 1140
142 ggatgagatt cagaatatga aggaggaaat ggctcgtcac cttcgtgaat accaagacct 1200
143 gctcaatgtt aagatggccc ttgacattga gattgccacc tacaggaagc tgctggaagg 1260
144 cgaggagagc aggatttctc tgcctcttcc aaacttttcc tccctgaacc tgagggaaac 1320
145 taatctggat tcactccctc tggttgatac ccactcaaaa aggacacttc tgattaagac 1380
146 ggttgaaact agagatggac aggttatcaa cgaaacttct cagcatcacg atgaccttga 1440
147 ataaaaattg cacacactca gtgcagcaat atattaccag caagaataaa aaagaaatcc 1500
148 atatcttaaa gaaacagctt tcaagtgcct ttctgcagtt tttcaggagc gcaagataga 1560
149 tttggaatag gaataagctc tagttcttaa caaccgacac tcctacaaga tttagaaaaa 1620
150 agtttacaac ataatctagt ttacagaaaa atcttgtgct agaatacttt ttaaaaggta 1680
151 ttttgaatac cattaanaact gctttttttt ttccagcaag tatccaacca acttggttct 1740
152 gcttcaataa atctttggaa aaacta 1766
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156 <211> LENGTH: 4
157 <212> TYPE: PRT
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160 <220> FEATURE:
161 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
162 linker peptide
164 <220> FEATURE:
165 <221> NAME/KEY: MOD_RES
166 <222> LOCATION: (4)
167 <223> OTHER INFORMATION: Leu-Dau
169 <400> SEQUENCE: 3
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171 1
174 <210> SEQ ID NO: 4
175 <211> LENGTH: 4
176 <212> TYPE: PRT
177 <213> ORGANISM: Artificial Sequence
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
181 linker peptide
183 <220> FEATURE:
184 <221> NAME/KEY: MOD_RES
185 <222> LOCATION: (4)
186 <223> OTHER INFORMATION: Gly-Dau
188 <400> SEQUENCE: 4
189 Gly Phe Leu Gly
190 1
193 <210> SEQ ID NO: 5
194 <211> LENGTH: 4
195 <212> TYPE: PRT

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196 <213> ORGANISM: Artificial Sequence
198 <220> FEATURE:
199 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
200 linker peptide
202 <400> SEQUENCE: 5
203 Leu Ala Leu Ala
204 1

VERIFICATION SUMMARY

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